

SEQUENCE LISTING

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The Regents of the University of California
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services

<120> Mammalian Sweet Taste Receptors

<130> 02307E-120110US

<140> US 09/927,315

<141> 2001-08-10

<150> US 60/302,898

<151> 2001-07-03

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 840

<212> PRT

<213> Rattus sp.

<220>

<223> rat T1R1 sweet taste receptor

<400> 1

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Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
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Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
35 40 45

Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
50 55 60

Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
65 70 75 80

Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
85 90 95

Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
100 105 110

Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile
115 120 125

Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
130 135 140

Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro
145 150 155 160

Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
165 170 175

Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
180 185 190

His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
195 200 205

Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
210 215 220

Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
225 230 235 240

Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
245 250 255

Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val
260 265 270

Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
275 280 285

Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
290 295 300

Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
305 310 315 320

Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
325 330 335

Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
340 345 350

Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
355 360 365

Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
370 375 380

Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
385 390 395 400

Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
405 410 415

Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
420 425 430

Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
435 440 445

Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
450 455 460

Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
465 470 475 480

Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
485 490 495

Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
500 505 510

His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
515 520 525

Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala
530 535 540

Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
545 550 555 560

Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
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Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His
580 585 590

Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
595 600 605

Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
610 615 620

Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
625 630 635 640

Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
645 650 655

Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
660 665 670

Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val
675 680 685

His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
690 695 700

Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
705 710 715 720

Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
725 730 735

Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
740 745 750

Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
755 760 765

Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
770 775 780

Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
785 790 795 800

Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
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Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp
820 825 830

Tyr Thr Arg Arg Cys Gly Thr Thr
835 840

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<211> 842

<212> PRT

<213> Mus musculus

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<223> mouse T1R1 sweet taste receptor

<400> 2

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20 25 30

Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His
35 40 45

Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp
50 55 60

Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met
65 70 75 80

Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
85 90 95

Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn
100 105 110

Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu
115 120 125

Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu
130 135 140

Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu
145 150 155 160

Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile
165 170 175

Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser
180 185 190

Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly
195 200 205

Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu
210 215 220

Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val
225 230 235 240

Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg
245 250 255

Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val
260 265 270

Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val
275 280 285

Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp
290 295 300

Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly
305 310 315 320

Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys
325 330 335

Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr
340 345 350

Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys
355 360 365

His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met
370 375 380

Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly
385 390 395 400

Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro
405 410 415

Val Tyr Pro Trp Gln Leu Leu Gln Ile Tyr Lys Val Asn Phe Leu
420 425 430

Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly
435 440 445

Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
450 455 460

Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn
465 470 475 480

Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser
485 490 495

Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly
500 505 510

Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe
515 520 525

Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu
530 535 540

Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe
545 550 555 560

Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr
565 570 575

Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg
580 585 590

Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu
595 600 605

Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe
610 615 620

Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser
625 630 635 640

Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln
645 650 655

Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His
660 665 670

Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser
675 680 685

Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro
690 695 700

Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu
705 710 715 720

Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn
725 730 735

Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu
740 745 750

Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu
755 760 765

Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr
770 775 780

Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr
785 790 795 800

Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile
805 810 815

Leu Cys Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile
820 825 830

Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr
835 840

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<212> PRT
<213> Homo sapiens

<220>
<223> human T1R1 sweet taste receptor

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Arg Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
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Ile Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn
35 40 45
Val Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile
50 55 60
Glu Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val
65 70 75 80
Ile Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu
85 90 95
Ser Pro Phe Leu Val His Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
100 105 110
Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
115 120 125
Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
130 135 140
Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
145 150 155 160
Val Gln Ala Leu Glu Asn Gln Ala Leu Val Arg Gly Ile Cys Ile Ala
165 170 175
Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
180 185 190
Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
195 200 205
Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
210 215 220
Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
225 230 235 240
Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
245 250 255

Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
260 265 270

Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Glu Ala Pro Arg Pro Cys
275 280 285

His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
290 295 300

Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
305 310 315 320

Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
325 330 335

His Gln Leu Leu Gly Cys Ala Ser Glu Leu Cys Ser Arg Gly Arg Val
340 345 350

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
355 360 365

His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
370 375 380

Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
385 390 395 400

Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
405 410 415

Thr Lys Ile Gln Trp His Gly Lys Asn His Gln Val Pro Lys Ser Val
420 425 430

Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
435 440 445

His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
450 455 460

Asn Lys Ser Glu Leu Tyr Arg Cys Gln Pro Cys Gly Thr Glu Glu Trp
465 470 475 480

Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
485 490 495

Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
500 505 510

Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
515 520 525

Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
530 535 540

Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
545 550 555 560

Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
565 570 575

Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
 580 585 590
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 595 600 605
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 610 615 620
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 625 630 635 640
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 645 650 655
 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
 660 665 670
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
 675 680 685
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
 690 695 700
 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
 705 710 715 720
 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
 725 730 735
 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
 740 745 750
 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
 755 760 765
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr
 770 775

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 <212> DNA
 <213> Rattus sp.

<220>
 <223> rat T1R1 sweet taste receptor

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 <213> Mus musculus

<220>
 <223> mouse T1R1 sweet taste receptor

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<220>
<223> human T1R1 sweet taste receptor

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<210> 7
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<212> PRT
<213> Rattus sp.

<220>
<223> rat T1R2 sweet taste receptor

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Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
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Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
50 55 60

Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile His
100 105 110

Pro Gly Leu Tyr Phe Leu Ala Gln Asp Asp Asp Asp Leu Leu Pro Ile Leu
115 120 125

Lys Asp Tyr Ser Gln Tyr Met Pro His Val Val Ala Val Ile Gly Pro
 130 135 140

Asp Asn Sér Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser His Phe
145 150 155 160

Leu Ile Pro Gln Ile Thr Tyr Ser Ala Ile Ser Asp Lys Leu Arg Asp
165 170 175

Lys Arg His Phe Pro Ser Met Leu Arg Thr Val Pro Ser Ala Thr His
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
210 215 220

Leu Leu Ser Gln Arg Leu Thr Lys Thr Ser Asp Ile Cys Ile Ala Phe
225 230 235 240

Gln Glu Val Leu Pro Ile Pro Glu Ser Ser Gln Val Met Arg Ser Glu
245 250 255

Glu Gln Arg Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
260 265 270

Ala Arg Val Val Val Val Phe Ser Pro Glu Leu Ser Leu Tyr Ser Phe
275 280 285

Phe His Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala
290 295 300

Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu
305 310 315 320

Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile
325 330 335

Pro Gly Phe Ser Gln Phe Arg Val Arg Arg Asp Lys Pro Gly Tyr Pro
340 345 350

Val Pro Asn Thr Thr Asn Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp
355 360 365

Ala Cys Leu Asn Thr Thr Lys Ser Phe Asn Asn Ile Leu Ile Leu Ser
370 375 380

Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
385 390 395 400

His Ala Leu His Arg Leu Leu Gly Cys Asn Arg Val Arg Cys Thr Lys
405 410 415

Gln Lys Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
420 425 430

Phe Thr Leu Leu Gly Asn Arg Leu Phe Phe Asp Gln Gln Gly Asp Met
435 440 445

Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Asp Leu Ser Gln Asn
450 455 460

Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Ser Lys Arg Leu Thr
465 470 475 480

Tyr Ile Asn Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Val
485 490 495

Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Ser Val
500 505 510

Gly Leu His Pro Cys Cys Phe Glu Cys Leu Asp Cys Met Pro Gly Thr
515 520 525

Tyr Leu Asn Arg Ser Ala Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
530 535 540

Ser Met Trp Ser Tyr Lys Asn Asp Ile Thr Cys Phe Gln Arg Arg Pro
545 550 555 560

Thr Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Ala Ile Leu
565 570 575

Ala Ala Leu Gly Phe Phe Ser Thr Leu Ala Ile Leu Phe Ile Phe Trp
580 585 590

Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
595 600 605

Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
610 615 620

Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
625 630 635 640

Phe Thr Val Cys Phe Ser Ile Cys Leu Ser Cys Ile Thr Val Arg Ser
645 650 655

Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
660 665 670

Tyr Ser Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
675 680 685

Ile Thr Ala Ile Lys Val Ala Leu Val Val Gly Asn Met Leu Ala Thr
690 695 700

Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Met
705 710 715 720

Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
725 730 735

Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Met
740 745 750

Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
755 760 765

Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
770 775 780

Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
785 790 795 800

Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
835 840

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<211> 843
<212> PRT
<213> Mus musculus

<220>
<223> mouse T1R2 sweet taste receptor

<400> 8
Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu His
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Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu
20 25 30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
50 55 60

Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln
100 105 110

Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu
115 120 125

Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro
130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe
145 150 155 160

Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp
165 170 175

Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
210 215 220

Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe
225 230 235 240

Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu
 245 250 255
 Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
 260 265 270
 Ala Arg Val Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe
 275 280 285
 Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala
 290 295 300
 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu
 305 310 315 320
 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile
 325 330 335
 Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Gly Tyr Arg
 340 345 350
 Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp
 355 360 365
 Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser
 370 375 380
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
 385 390 395 400
 His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys
 405 410 415
 Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
 420 425 430
 Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met
 435 440 445
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn
 450 455 460
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr
 465 470 475 480
 Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile
 485 490 495
 Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile
 500 505 510
 Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Asp Thr
 515 520 525
 Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
 530 535 540
 Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu
 545 550 555 560

Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu
 565 570 575
 Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp
 580 585 590
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
 595 600 605
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
 610 615 620
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
 625 630 635 640
 Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser
 645 650 655
 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
 660 665 670
 Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
 675 680 685
 Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr
 690 695 700
 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile
 705 710 715 720
 Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
 725 730 735
 Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val
 740 745 750
 Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
 755 760 765
 Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
 770 775 780
 Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
 785 790 795 800
 Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
 805 810 815
 Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
 820 825 830
 Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
 835 840

<210> 9
 <211> 838
 <212> PRT
 <213> Homo sapiens

<220>

<223> human T1R2 sweet taste receptor

<400> 9

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
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Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
20 25 30

Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
35 40 45

Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
50 55 60

Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
65 70 75 80

Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
85 90 95

Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
100 105 110

Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
115 120 125

Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
130 135 140

Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
145 150 155 160

Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
165 170 175

Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu
180 185 190

Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val
195 200 205

Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly
210 215 220

Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
225 230 235 240

Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg
245 250 255

Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
260 265 270

Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val
275 280 285

Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
290 295 300

Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly
 305 310 315 320
 Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
 325 330 335
 Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
 340 345 350
 Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
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 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Leu Gly
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 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
 580 585 590
 Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605
 Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620

Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
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 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655
 Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Arg Pro Gln Ser His
 690 695 700
 Pro Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys Asn
 705 710 715 720
 Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu Leu
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 Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu Pro
 740 745 750
 Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe Tyr
 755 760 765
 Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser Gly
 770 775 780
 Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu Leu
 785 790 795 800
 Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu Phe
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 Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln Gly
 820 825 830
 Tyr Thr Met Arg Arg Asp
 835

<210> 10
 <211> 2993
 <212> DNA
 <213> Rattus sp.

<220>
 <223> rat T1R2 sweet taste receptor

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 aaacttccctt ccggtaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2993

<210> 11
 <211> 2532
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse T1R2 sweet taste receptor

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Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
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Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
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Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
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Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
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Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
35 40 45

Ala Thr Leu Asn Gln Arg Ala Gln Pro Asn Ser Thr Leu Cys Asn Arg
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Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
100 105 110

Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
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Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
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Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
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Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
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Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
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His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
325 330 335

Tyr Val Glu Thr His Leu Ala Leu Ala Asp Pro Ala Phe Cys Ala
340 345 350

Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg
355 360 365

Cys Pro Gln Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
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Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
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Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala
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Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
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Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser
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Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu
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Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr
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Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
725 730 735

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755 760 765

Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val
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Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
785 790 795 800

Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
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Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
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 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
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 Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
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 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
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 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
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 Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
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Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
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Tyr Val Glu Thr His Leu Ala Leu Ala Ala Asp Pro Ala Phe Cys Ala
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Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg
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Cys Pro Gln Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
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Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
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 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
 725 730 735
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
 740 745 750
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 755 760 765
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val
 770 775 780
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
 785 790 795 800
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
 820 825 830
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly
 835 840 845
 Gly Gly Glu Ala Ala Gln Glu His Asn Glu
 850 855

<210> 21
 <211> 3200
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse Sac taster C57 T1R3 sweet taste receptor
 genomic

<400> 21
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 tgggttctca accgattgca cccattgagc tctcatatca gaaagtgtt cttgatcacc 720
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<210> 22
 <211> 2577
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse Sac taster C57 T1R3 sweet taste receptor CDS

<400> 22
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gaggagatca acaaatggatc tgccttgctc cctggggctgc ggctgggcta tgaccttattt 300
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<210> 23

<211> 858

<212> PRT

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor

<400> 23

Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu
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Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
20 25 30

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Pro Cys Asn Arg
50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
100 105 110

Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
180 185 190

Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
245 250 255

Leu Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
260 265 270

Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
275 280 285

His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
325 330 335

Tyr Val Glu Thr His Leu Ala Leu Ala Ala Asp Pro Ala Phe Cys Ala
340 345 350

Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg
355 360 365

Cys Pro Arg Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
370 375 380

Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
385 390 395 400

Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
405 410 415

Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
420 425 430

Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr
435 440 445

Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys
450 455 460

Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
465 470 475 480

Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly
485 490 495

Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
500 505 510

Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
515 520 525

Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
530 535 540

Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu
545 550 555 560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser
565 570 575

Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Leu
580 585 590

Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
595 600 605

Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
610 615 620

Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala
625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
645 650 655

Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser
660 665 670

Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu
675 680 685

Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr
690 695 700

Leu Ile Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro
 705 710 715 720
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
 725 730 735
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
 740 745 750
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 755 760 765
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val
 770 775 780
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
 785 790 795 800
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
 820 825 830
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly
 835 840 845
 Gly Gly Glu Ala Ala Gln Gly His Asn Glu
 850 855

<210> 24
 <211> 2577
 <212> DNA
 <213> Rattus sp.

<220>
 <223> rat T1R3 sweet taste receptor CDS

<400> 24
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<210> 25
<211> 858
<212> PRT
<213> *Rattus* sp.

<220>
<223> rat T1R3 sweet taste receptor

<400> 25
Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu
1 5 10 15

Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
20 25 30

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
 100 105 110

Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
180 185 190

Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
245 250 255

Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
260 265 270

Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
275 280 285

Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
325 330 335

Tyr Val Glu Thr Arg Leu Ala Leu Ala Asp Pro Thr Phe Cys Ala
340 345 350

Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg
355 360 365

Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
370 375 380

Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
385 390 395 400

Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
405 410 415

Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
420 425 430

Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
435 440 445

Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
450 455 460

Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
465 470 475 480

Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly
485 490 495

Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
500 505 510

Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
515 520 525

Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
530 535 540

Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
545 550 555 560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
565 570 575

Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
580 585 590

Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
595 600 605

Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
610 615 620

Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
645 650 655

Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
660 665 670

Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
675 680 685

Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
690 695 700

Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
705 710 715 720

Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
725 730 735

Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
740 745 750

Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
755 760 765

Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
770 775 780

Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
785 790 795 800

Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu
805 810 815

Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu
820 825 830

Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly
835 840 845

Ser Ser Glu Ala Thr Arg Gly His Ser Glu
850 855